OIPE

RAW SEQUENCE LISTING   DATE: 02/16/2002
PATENT APPLICATION: US/10/068,080   TIME: 13:17:21

Input Set : N:\Crf3\RULE60\10068080.txt
Output Set: N:\CRF3\02152002\J068080.raw

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 4 <110> APPLICANT: Fritz, Christian
 5         Youngman, Philip
 7 <120> TITLE OF INVENTION: USE OF YNES, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
 9 <130> FILE REFERENCE: 07334/090001
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/068,080
    12 <141> CURRENT FILING DATE: 2002-02-05
W--> 14 <140> CURRENT APPLICATION NUMBER: US 09/163,445
    15 <141> CURRENT FILING DATE: 1998-09-30
    18 <150> PRIOR APPLICATION NUMBER: US 60/070,116
    19 <151> PRIOR FILING DATE: 1997-12-31
    21 <160> NUMBER OF SEQ ID NOS: 12
    23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
    25 <210> SEQ ID NO: 1
    26 <211> LENGTH: 213
    27 <212> TYPE: PRT
    28 <213> ORGANISM: Streptococcus pneumoniae
    30 <400> SEQUENCE: 1
    31 Met Ile Thr Ile Val Leu Leu Ile Leu Ala Tyr Leu Leu Gly Ser Ile
    32  1               5                  10                  15
    33 Pro Ser Gly Leu Trp Ile Gly Gln Val Phe Phe Gln Ile Asn Leu Arg
    34              20                  25                  30
    35 Glu His Gly Ser Gly Asn Thr Gly Thr Thr Asn Thr Phe Arg Ile Leu
    36          35                  40                  45
    37 Gly Lys Lys Ala Gly Met Ala Thr Phe Val Ile Asp Phe Phe Lys Gly
    38       50                  55                  60
    39 Thr Leu Ala Thr Leu Leu Pro Ile Ile Phe His Leu Gln Gly Val Ser
    40  65                  70                  75                  80
    41 Pro Leu Ile Phe Gly Leu Leu Ala Val Ile Gly His Thr Phe Pro Ile
    42              85                  90                  95
    43 Phe Ala Gly Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Ala Gly Val
    44              100                 105                 110
    45 Ile Phe Gly Phe Ala Pro Ile Phe Cys Leu Tyr Leu Ala Ile Ile Phe
    46          115                 120                 125
    47 Phe Gly Ala Leu Tyr Leu Gly Ser Met Ile Ser Leu Ser Ser Val Thr
    48       130                 135                 140
    49 Ala Ser Ile Ala Ala Val Ile Gly Val Leu Leu Phe Pro Leu Phe Gly
    50 145                 150                 155                 160
    51 Phe Ile Leu Ser Asn Tyr Asp Ser Leu Phe Ile Ala Ile Ile Leu Ala
    52              165                 170                 175
    53 Leu Ala Ser Leu Ile Ile Ile Arg His Lys Asp Asn Ile Ala Arg Ile
    54              180                 185                 190
    55 Lys Asn Lys Thr Glu Asn Leu Val Pro Trp Gly Leu Asn Leu Thr His
    56          195                 200                 205
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57   Gln Asp Pro Lys Lys
58       210
60  <210> SEQ ID NO: 2
61  <211> LENGTH: 642
62  <212> TYPE: DNA
63  <213> ORGANISM: Streptococcus pneumoniae
65  <220> FEATURE:
66  <221> NAME/KEY: CDS
67  <222> LOCATION: (1)...(639)
71  <400> SEQUENCE: 2
72   atg att aca ata gtt tta tta atc cta gcc tat ctg ctg ggt tcg att        48
73   Met Ile Thr Ile Val Leu Leu Ile Leu Ala Tyr Leu Leu Gly Ser Ile
74    1              5                   10                  15
76   cca tct ggt ctc tgg att gga caa gta ttc ttt caa atc aat cta cgc        96
77   Pro Ser Gly Leu Trp Ile Gly Gln Val Phe Phe Gln Ile Asn Leu Arg
78               20                  25                  30
80   gag cat ggt tct ggt aac act gga acg acc aac acc ttc cgc att tta       144
81   Glu His Gly Ser Gly Asn Thr Gly Thr Thr Asn Thr Phe Arg Ile Leu
82           35                  40                  45
84   ggt aag aaa gct ggt atg gca acc ttt gtg att gac ttt ttc aaa gga       192
85   Gly Lys Lys Ala Gly Met Ala Thr Phe Val Ile Asp Phe Phe Lys Gly
86       50                  55                  60
88   acc cta gca acg ctg ctt ccg att att ttt cat cta caa ggc gtt tct       240
89   Thr Leu Ala Thr Leu Leu Pro Ile Ile Phe His Leu Gln Gly Val Ser
90    65                  70                  75                  80
92   cct ctc atc ttt gga ctt ttg gct gtt atc ggc cat acc ttc cct atc       288
93   Pro Leu Ile Phe Gly Leu Leu Ala Val Ile Gly His Thr Phe Pro Ile
94                       85                  90                  95
96   ttt gca gga ttt aaa ggt ggt aag gct gtc gca acc agt gct gga gtg       336
97   Phe Ala Gly Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Ala Gly Val
98                100                 105                 110
100  att ttc gga ttt gcg cct atc ttc tgt ctc tac ctt gcg att atc ttc       384
101  Ile Phe Gly Phe Ala Pro Ile Phe Cys Leu Tyr Leu Ala Ile Ile Phe
102          115                 120                 125
104  ttt gga gct ctc tat ctt ggc agt atg att tca ctg tct agt gtc aca       432
105  Phe Gly Ala Leu Tyr Leu Gly Ser Met Ile Ser Leu Ser Ser Val Thr
106         130                 135                 140
108  gca tcg att gcg gct gtt atc ggg gtt ctg ctc ttt cca ctt ttt ggt       480
109  Ala Ser Ile Ala Ala Val Ile Gly Val Leu Leu Phe Pro Leu Phe Gly
110  145                 150                 155                 160
112  ttt atc ctg agt aac tat gac tct ctc ttc atc gct att atc tta gca       528
113  Phe Ile Leu Ser Asn Tyr Asp Ser Leu Phe Ile Ala Ile Ile Leu Ala
114                  165                 170                 175
116  ctt gct agt ttg att atc att cgt cat aag gac aat ata gct cgt atc       576
117  Leu Ala Ser Leu Ile Ile Ile Arg His Lys Asp Asn Ile Ala Arg Ile
118                  180                 185                 190
120  aaa aat aaa act gaa aat ttg gtc cct tgg gga ttg aac cta acc cat       624
121  Lys Asn Lys Thr Glu Asn Leu Val Pro Trp Gly Leu Asn Leu Thr His
122             195                 200                 205
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124  caa gat cct aaa aaa taa                                      642
125  Gln Asp Pro Lys Lys
126      210
128 <210> SEQ ID NO: 3
129 <211> LENGTH: 193
130 <212> TYPE: PRT
131 <213> ORGANISM: Streptococcus pneumoniae
135 <400> SEQUENCE: 3
136  Met Leu Ile Ala Leu Leu Ile Ile Leu Ala Tyr Leu Ile Gly Ser Ile
137   1               5                  10                  15
138  Pro Ser Gly Leu Ile Val Gly Lys Leu Ala Lys Gly Ile Asp Ile Arg
139              20 .               25                  30
140  Glu His Gly Ser Gly Asn Leu Gly Ala Thr Asn Ala Phe Arg Thr Leu
141          35                  40                  45
142  Gly Val Lys Ala Gly Ser Val Val Ile Ala Gly Asp Ile Leu Lys Gly
143          50                  55                  60
144  Thr Leu Ala Thr Ala Leu Pro Phe Leu Met His Val Asp Ile His Pro
145   65                  70                  75                  80
146  Leu Leu Ala Gly Val Phe Ala Val Leu Gly His Val Phe Pro Ile Phe
147                  85                  90 .                  95
148  Ala Lys Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Gly Gly Val Leu
149              100                 105                 110
150  Leu Phe Tyr Ala Pro Leu Leu Phe Ile Thr Met Val Ala Val Phe Phe
151          115                 120 ·                 125
152  Ile Phe Leu Tyr Leu Thr Lys Phe Val Ser Leu Ser Ser Met Leu Thr
153 ·       130                 135         .           140
154  Gly Ile Tyr Thr Val Ile Tyr Ser Phe Phe Val His Asp Thr Tyr Leu
155  145                 150                 155 .                160
156  Leu Ile Val Val Thr Leu Leu Thr Ile Phe Val Ile Tyr Arg His Arg
157                  165                 170                 175
158  Ala Asn Ile Lys Arg Ile Ile Asn Lys Thr Glu Pro Lys Val Lys Trp
159              180                 185                 190
160  Leu
163 <210> SEQ ID NO: 4
164 <211> LENGTH: 582
165 <212> TYPE: DNA
166 <213> ORGANISM: Streptococcus pneumoniae
168 <220> FEATURE:
169 <221> NAME/KEY: CDS
170 <222> LOCATION: (1)...(579)
172 <400> SEQUENCE: 4
173  atg tta att gct tta ttg att att ttg gcc tac ttg ata ggc agc att    48
174  Met Leu Ile Ala Leu Leu Ile Ile Leu Ala Tyr Leu Ile Gly Ser Ile
175   1               5                  10                  15
177  cca tct ggc tta att gtg ggc aag ctt gcc aaa gga att gat att cgg    96
178  Pro Ser Gly Leu Ile Val Gly Lys Leu Ala Lys Gly Ile Asp Ile Arg
179              20                  25                  30
181  gag cac gga agc ggc aac tta ggc gct acc aat gca ttc cgt aca ttg   144
182  Glu His Gly Ser Gly Asn Leu Gly Ala Thr Asn Ala Phe Arg Thr Leu
```

```
183           35                    40                    45
185   ggt gta aaa gct ggt tcg gtc gtc ata gcc gga gat att ttg aaa ggg        192
186   Gly Val Lys Ala Gly Ser Val Val Ile Ala Gly Asp Ile Leu Lys Gly
187        50                    55                    60
189   aca ctg gca act gca ttg cct ttt ctc atg cat gtt gat att cac ccg        240
190   Thr Leu Ala Thr Ala Leu Pro Phe Leu Met His Val Asp Ile His Pro
191     65                    70                    75                    80
193   ctt ctt gca gga gtc ttt gcg gtt tta ggc cac gtg ttt ccc atc ttc        288
194   Leu Leu Ala Gly Val Phe Ala Val Leu Gly His Val Phe Pro Ile Phe
195                    85                    90                    95
199   gcc aaa ttt aaa ggc ggt aaa gcc gtg gcg aca tca gga ggc gtt ttg        336
200   Ala Lys Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Gly Gly Val Leu
201              100                   105                   110
203   cta ttt tac gca ccc ctg tta ttt atc acg atg gtt gcg gta ttc ttc        384
204   Leu Phe Tyr Ala Pro Leu Leu Phe Ile Thr Met Val Ala Val Phe Phe
205           115                   120                   125
207   atc ttt tta tac ttg act aaa ttt gtt tct ctc tca tcg atg tta aca        432
208   Ile Phe Leu Tyr Leu Thr Lys Phe Val Ser Leu Ser Ser Met Leu Thr
209        130                   135                   140
211   ggg atc tat act gtt ata tat agt ttc ttt gtc cat gat acg tat tta        480
212   Gly Ile Tyr Thr Val Ile Tyr Ser Phe Phe Val His Asp Thr Tyr Leu
213   145                   150                   155                   160
215   ttg att gtc gtt acc ctg ctc act att ttt gtg ata tac aga cac cga        528
216   Leu Ile Val Val Thr Leu Leu Thr Ile Phe Val Ile Tyr Arg His Arg
217                    165                   170                   175
219   gcg aac att aaa cga att atc aat aaa aca gaa cct aaa gta aaa tgg        576
220   Ala Asn Ile Lys Arg Ile Ile Asn Lys Thr Glu Pro Lys Val Lys Trp
221              180                   185                   190
223   tta taa                                                                582
224   Leu
227   <210> SEQ ID NO: 5
228   <211> LENGTH: 21
229   <212> TYPE: DNA
230   <213> ORGANISM: B. subtilis
232   <400> SEQUENCE: 5
233    gtgttcgtgc tgacttgcac c                                                21
235   <210> SEQ ID NO: 6
236   <211> LENGTH: 21
237   <212> TYPE: DNA
238   <213> ORGANISM: B. subtilis
240   <400> SEQUENCE: 6
241    gaattatttc ctcccgttaa a                                                21
243   <210> SEQ ID NO: 7
244   <211> LENGTH: 21
245   <212> TYPE: DNA
246   <213> ORGANISM: Steptococcus pneumoniae
248   <400> SEQUENCE: 7
249    acccactccg tgaagtccac c                                                21
251   <210> SEQ ID NO: 8
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252 <211> LENGTH: 21
253 <212> TYPE: DNA
254 <213> ORGANISM: Streptococcus pneumoniae
256 <400> SEQUENCE: 8
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259 <210> SEQ ID NO: 9
260 <211> LENGTH: 21
263 <212> TYPE: DNA
264 <213> ORGANISM: Steptococcus pneumoniae
266 <400> SEQUENCE: 9
267  gaacctaacc catcaagatc c                                          21
269 <210> SEQ ID NO: 10
270 <211> LENGTH: 24
271 <212> TYPE: DNA
272 <213> ORGANISM: Streptococcus pneumoniae
274 <400> SEQUENCE: 10
275  cagttttaga tggctttaac agcg                                       24
277 <210> SEQ ID NO: 11
278 <211> LENGTH: 642
279 <212> TYPE: DNA
280 <213> ORGANISM: Streptococcus pneumoniae
282 <400> SEQUENCE: 11
283  tactaatgtt atcaaataa ttaggatcgg atagacgacc caagctaagg tagaccagag    60
284  acctaacctg ttcataagaa agtttagtta gatgcgctcg taccaagacc attgtgacct   120
285  tgctggttgt ggaaggcgta aaatccattc tttcgaccat accgttggaa acactaactg   180
286  aaaaagtttc cttgggatcg ttgcgacgaa ggctaataaa aagtagatgt tccgcaaaga   240
287  ggagagtaga aacctgaaaa ccgacaatag ccggtatgga agggatagaa acgtcctaaa   300
288  tttccaccat tccgacagcg ttggtcacga cctcactaaa agcctaaacg cggatagaag   360
289  acagagatgg aacgctaata gaagaaacct cgagagatag aaccgtcata ctaaagtgac   420
290  agatcacagt gtcgtagcta acgccgacaa tagccccaag acgagaaagg tgaaaaacca   480
291  aaataggact cattgatact gagagagaag tagcgataat agaatcgtga acgatcaaac   540
292  taatagtaag cagtattcct gttatatcga gcatagtttt tattttgact tttaaaccag   600
293  ggaacccta acttggattg ggtagttcta ggattttta tt                       642
295 <210> SEQ ID NO: 12
296 <211> LENGTH: 582
297 <212> TYPE: DNA
298 <213> ORGANISM: Streptococcus pneumoniae
300 <400> SEQUENCE: 12
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303  cgatggttac gtaaggcatg taacccacat tttcgaccaa gccagcagta tcggcctcta   180
304  taaaactttc cctgtgaccg ttgacgtaac ggaaaagagt acgtacaact ataagtgggc   240
305  gaagaacgtc ctcagaaacg ccaaaatccg gtgcacaaag ggtagaagcg gtttaaattt   300
306  ccgccatttc ggcaccgctg tagtcctccg caaaacgata aaatgcgtgg ggacaataaa   360
307  tagtgctacc aacgccataa gaagtagaaa aatatgaact gatttaaaca aagagagagt   420
308  agctacaatt gtccctagat atgacaatat atatcaaaga aacaggtact atgcataaat   480
309  aactaacagc aatgggacga gtgataaaaa cactatatgt ctgtggctcg cttgtaattt   540
310  gcttaatagt tattttgtct tggatttcat tttaccaata tt                     582
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VERIFICATION SUMMARY   DATE: 02/16/2002
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Input Set : **N:\Crf3\RULE60\10068080.txt**
Output Set: **N:\CRF3\02152002\J068080.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:280 W: Numeric Identifier already exists, <140> found multiple times
L:14 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:320 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12